

APPENDIX B
SUBSTITUTE SHEETS



Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	SEQ ID	Sequence	Binding Affinity (nM)
DRB1*0101	DR1	515.01	2128	PKYVKQNTLKLAT	5.0
DRB1*0301	DR3	829.02	2129	YKTIAFDEEARR	300
DRB1*0401	DR4w4	515.01	2130	PKYVKQNTLKLAT	45
DRB1*0404	DR4w14	717.01	2131	YARFQSQTTLKQKT	50
DRB1*0405	DR4w15	717.01	2132	YARFQSQTTLKQKT	38
DRB1*0701	DR7	553.01	2133	QYIKANSKFIGITE	25
DRB1*0802	DR8w2	553.01	2134	QYIKANSKFIGITE	49
DRB1*0803	DR8w3	553.01	2135	QYIKANSKFIGITE	1600
DRB1*0901	DR9	553.01	2136	QYIKANSKFIGITE	75
DRB1*1101	DR5w11	553.01	2137	QYIKANSKFIGITE	20
DRB1*1201	DR5w12	1200.05	2138	EALIHQLKINPYVLS	298
DRB1*1302	DR6w19	650.22	2139	QYIKANAKFIGITE	3.5
DRB1*1501	DR2w2 β 1	507.02	2140	GRTQDENPVVHFFK NIVTPRTPPP	9.1
DRB3*0101	DR52a	511	2141	NGQIGNDPNRDIL	470
DRB4*0101	DRw53	717.01	2142	YARFQSQTTLKQKT	58
DRB5*0101	DR2w2 β 2	553.01	2143	QYIKANSKFIGITE	20

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

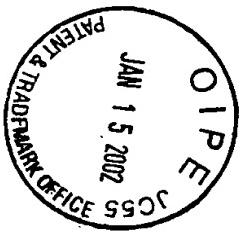


Table XIX
CEA DR Super Motif Peptides with

Core Sequence	Core SeqId Num	Exemplary Sequence	Exemplary SeqId Num	Position	DR1	DR2w β 1	DR2w β 2	DR3	DR4w4	DR4w5	DR5w11	DR5w12
IPWORLLT WORLLTAS	1962 1963	RWCIPWORLLTASL CIPWORLLTASLT	1815 1816	10 12	0.6100 0.0110	-0.0007 0.0150	0.0830 0.0830				-0.0006 -0.0022	
LL,T,ASL,T LT,ASL,TF	1964 1965	WCRLL,TASHLTFWN QRLTASLLTFWNP	1817 1818	15 16	-0.0004 -0.0004						-0.0022 -0.0022	
LT,ASL,TFW LT,FWNPPTT	1966 1967	RLL,TASL,TFWNPP ASLLTFWNPPTAKL	1819 1820	17 22							-0.0005 -0.0005	
FWNPPTTAK WNPPTTAKL	1968 1969	LJ,TEWNPPTTAKLTI LT,FWNPPTTAKLTI	1821 1822	24 25							0.0340 0.0340	
L,T,TESTPN LL,VHN,POH	1970 1971	TAKL,TTESTPNVAF EVLL,VHN,POHLFG	1823 1824	33 30								
L,VHN,POH, YKGERV,DGN	1972 1973	VLL,I,VHN,POH,FGY YSWYKGERV,DGNRQI	1825 1826	51 65								
IGVIGCTO IGTOA,TPG	1974 1975	NRQIVGIVGCTOQAT GYVIGTOQATPGPAY	1827 1828	76 81								
YSGRFLYYP IYPNASSL	1976 1977	GPA,YSGRFELYPNAS GREIYPNASSLJUN	1829 1830	92 98							0.0029 0.0029	
IYPNASSL,I YPNASSL,IJO	1978 1979	REIYPNASSLJUNI EIYPNASSLJUNII	1831 1832	100 99							-0.0005 -0.0005	
LLIONIJON LJONIJOND	1980 1981	NASLLIONIJONDTG ASLLIONIJONDTGF	1833 1834	104 105							-0.0022 -0.0022	
KDNTDFRY FTYLHVIKS	1982 1983	IONIJONDTCFYTLH DTGFTYTLHVIKSDLV	1835 1836	109 116							0.0080 0.0080	
YTL,HVIKSD LHVIKSDLV	1984 1985	TGF,YTL,HVIKSDI,VN FTYTLHVIKSDLVNEE	1837 1838	117 119								
VIKSDLVNE IKSDLVNEE	1986 1987	TLHVIKSDLVNEEAT LHVIKSDLVNEEATG	1839 1840	121 122							0.1300 0.0058	
I,VNF,FEATCO VNEEATCOF	1988 1989	KSDI,VNEEATGOFRV SDLVEEEATGOFRVY	1841 1842	126 127							- -	
VYPEL,PKPS LPKPSISSN	1990 1991	QF,RVYPEL,PKPSISS YELPKPSISSNSK	1843 1844	137 141							-0.0022 -0.0022	
ISSNN,SKPV VEDKDA,VAF	1992 1993	KPSISSNNNSKPVEDK SKPVEDKDA,VAFTE	1845 1846	146 154							-0.0022 -0.0022	
WVNNSOL,PF VNNNSLP,S	1994 1995	YI,WWVNNNSPVSPR LWWVNNSOLPVSPLR	1847 1848	176 177							0.7000 0.0290	
I,TI,TFNVTTRN VTRND,TASY	1996 1997	NRTL,TFNVTTRNTA LFWNVTTRNTASYKCE	1849 1850	197 202								
V,SARR,SDSV VILNVL,YGP	1998 1999	ONPV,SARR,SDSVLN SDSVILNVL,YGP,DAP	1851 1852	218 226								
I,YGP,DAP,TI I,TFNVTTRN	2000 2001	I,NVLYGP,DAP,TISPL NVLYGP,DAP,TISPLN	1853 1854	231 232								
ISPLNTSYR LSCHA,ASNP	2002 2003	APTISPLNTSYRSGE NLNSCHA,ASNP,OAO	1855 1856	239 254								
WFVN,GTFCO VTPNIT,VN	2004 2005	OYSWFVNGTFOOSTO TQFLNIP,TVNNSG	1857 1858	268 281								
FIPNIT,VNN IPNIT,VNN	2006 2007	QFL,FIPNIT,VNNSG ELFIPNIT,VNNSGSY	1859 1860	282 283								
ITVNNSGSY VNNSSGTYC	2008 2009	IPNIT,VNNSGSYTC NIT,VNNNSGTYCOAH	1861 1862	286 288								
LNRT,TTVTI VTTITVAYE	2010 2011	DTGLNRT,TTVTITV RTT,TTVTITV,AEPPK	1863 1864	305 310							-0.0004 -0.0004	
VYAFPK,PF ITSNN,SNPV	2012 2013	TTVYAFPPK,PFTS KPTTSNN,SNP,VEDE	1865 1866	315 324							0.0042 -0.0042	
VEDFDA,VAI LTL,SVTRN	2014 2015	SNP,VEDFDA,VAI,TC NRTL,TL,SVTRND,VG	1867 1868	332 375							0.0054 -0.0054	
VTRND,VGPY VGPY,EGCG	2016 2018	LLSVTRND,VGPY,EGCG EGCG,NE,SVDH,SDP	1869 1871	380 392							0.0210 0.0210	

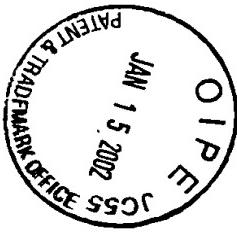


Table XIX
CEA DR Super Motif Peptides with

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DRI	DR2w β 1	DR2w β 2	DR3	DR4w4	DR4w5	DR5w11	DR5w12
L5VDHSDPV VDHSDPVIL VII.NVI.YGP YGPDDDTIS YTYRRGVN YYRPGVNL.S VNLSLSCHA I.SCHAASNP LJDGNIOQH I.FISNITFK FISNITEKN ITEKNSGIL LYTCQANNS VKTTVSAE VSAELPKPS WVNGOSLPV VNGOSLPVS LTLFNTRN VTRNDRAY IONSVSNR VSANRSDPV VTLDVLYGP LYGPDTPII YGPDTPII ISPDDSSYI. LSGANLNLS I.SCHAS.SNP IPOOHTIVL LFIAKITPN IAKITPNIN YACFVNLA FVNLSLATGR VSNLATGRN IVKSITVSA ITVSAGTS VSAGTSPG LSAGATVGI IMIGVLVGV LTIESPFN YKGFRVDG LPVSPRLQL I.NI.SCHAAS LPVSPRLQL	20119 20200 20221 20222 20223 20224 20225 20226 20227 20228 20229 20230 20231 20232 20233 20234 20235 20236 20237 20238 20239 20240 20241 20242 20243 20244 20245 20246 20247 20248 20249 20250 20251 20252 20253 20254 20255 20256 20257 20258 20259 20260 20261 20262 20263 20264 20265 20266	ONELSVDHSDPVILN EL5VDHSDPVILN SDP5VILNVL.YCPDDP NVLYGPDDDTISPSY DPTISPSYTYYRPG SPTYTYRPGVNLSL SYTYRPGVNLSLSC RPGVNLSSLSCHA NLSSLSCHAASNPA YSWLSDGNOOHTOE TOFL.FISNITEKNSG OLFISNITEKNSGL ISNITEKNSGILYCG NSGLYTTCOANNNSAG RTTVKTITVSAELPK TITVSAELPKPSISS SAELPKPSISSNSK YLWWVNGOSLPVSPR LWWVNGOSLPVSPRL NRLLTLEFNVRNDAR I.FNVRNDRAYVCG VCGIONSVAARSDP ONSVAARSDPVTLID SDPVTLIDDVLYCPDTP LDLVLYCPDTPISPP DVLVYCPDTPISPPD TPISPPDSSYLSAGA SSYLSGANLNLSCHS NLNLSCHSASNSPO OYSWRINGPOOHTO INGIPOOHTOVLIA TOVLEIAKITPNING OVLIAKITPNINGIT VLEIAKITPNINGIT NCYTACFVNLA.TGTR YACFVNLSLATGRNNS ACFVNLSLATGRNNSI NNSVKSITVSA.GST NSTVKSITVSA.GSTS VKSITVSA.GSTS.PG SITVVSAGTSPG.SA SPGLSAGATVGI.MIG TVMIGMIGVLVGV.MIG TAKLTIESTPENVVAE YSWYKCTERVDG.NRQI NCSLPVSPRLQLSNG GENI.NI.SCHAAS.NPP GOSLPPVSPRLQLSNG	1872 1873 1874 1875 1876 1877 1878 1879 1880 1881 1882 1883 1884 1885 1886 1887 1888 1889 1890 1891 1892 1893 1894 1895 1896 1897 1898 1899 1900 1901 1902 1903 1904 1905 1906 1907 1908 1909 1910 1911 1912 1913 1914 1915 1916 1917 1918 1919	0.0820 0.0820 396 398 404 410 417 421 423 428 432 447 459 460 0.0005 0.0180 464 471 488 493 497 499 532 533 553 558 570 574 582 587 588 595 603 610 624 629 637 638 639 650 653 654 665 666 669 671 680 688 693 699 707 713 722 730 738 746 754 762 770 778 786 794 802 810 818 826 834 842 850 858 866 874 882 890 898 906 914 922 930 938 946 954 962 970 978 986 994 1002 1010 1018 1026 1034 1042 1050 1058 1066 1074 1082 1090 1098 1106 1114 1122 1130 1138 1146 1154 1162 1170 1178 1186 1194 1202 1210 1218 1226 1234 1242 1250 1258 1266 1274 1282 1290 1298 1306 1314 1322 1330 1338 1346 1354 1362 1370 1378 1386 1394 1402 1410 1418 1426 1434 1442 1450 1458 1466 1474 1482 1490 1498 1506 1514 1522 1530 1538 1546 1554 1562 1570 1578 1586 1594 1602 1610 1618 1626 1634 1642 1650 1658 1666 1674 1682 1690 1698 1706 1714 1722 1730 1738 1746 1754 1762 1770 1778 1786 1794 1802 1810 1818 1826 1834 1842 1850 1858 1866 1874 1882 1890 1898 1906 1914 1922 1930 1938 1946 1954 1962 1970 1978 1986 1994 2002 2010 2018 2026 2034 2042 2050 2058 2066 2074 2082 2090 2098 2106 2114 2122 2130 2138 2146 2154 2162 2170 2178 2186 2194 2202 2210 2218 2226 2234 2242 2250 2258 2266 2274 2282 2290 2298 2306 2314 2322 2330 2338 2346 2354 2362 2370 2378 2386 2394 2402 2410 2418 2426 2434 2442 2450 2458 2466 2474 2482 2490 2498 2506 2514 2522 2530 2538 2546 2554 2562 2570 2578 2586 2594 2602 2610 2618 2626 2634 2642 2650 2658 2666 2674 2682 2690 2698 2706 2714 2722 2730 2738 2746 2754 2762 2770 2778 2786 2794 2802 2810 2818 2826 2834 2842 2850 2858 2866 2874 2882 2890 2898 2906 2914 2922 2930 2938 2946 2954 2962 2970 2978 2986 2994 3002 3010 3018 3026 3034 3042 3050 3058 3066 3074 3082 3090 3098 3106 3114 3122 3130 3138 3146 3154 3162 3170 3178 3186 3194 3202 3210 3218 3226 3234 3242 3250 3258 3266 3274 3282 3290 3298 3306 3314 3322 3330 3338 3346 3354 3362 3370 3378 3386 3394 3402 3410 3418 3426 3434 3442 3450 3458 3466 3474 3482 3490 3498 3506 3514 3522 3530 3538 3546 3554 3562 3570 3578 3586 3594 3602 3610 3618 3626 3634 3642 3650 3658 3666 3674 3682 3690 3698 3706 3714 3722 3730 3738 3746 3754 3762 3770 3778 3786 3794 3802 3810 3818 3826 3834 3842 3850 3858 3866 3874 3882 3890 3898 3906 3914 3922 3930 3938 3946 3954 3962 3970 3978 3986 3994 4002 4010 4018 4026 4034 4042 4050 4058 4066 4074 4082 4090 4098 4106 4114 4122 4130 4138 4146 4154 4162 4170 4178 4186 4194 4202 4210 4218 4226 4234 4242 4250 4258 4266 4274 4282 4290 4298 4306 4314 4322 4330 4338 4346 4354 4362 4370 4378 4386 4394 4402 4410 4418 4426 4434 4442 4450 4458 4466 4474 4482 4490 4498 4506 4514 4522 4530 4538 4546 4554 4562 4570 4578 4586 4594 4602 4610 4618 4626 4634 4642 4650 4658 4666 4674 4682 4690 4698 4706 4714 4722 4730 4738 4746 4754 4762 4770 4778 4786 4794 4802 4810 4818 4826 4834 4842 4850 4858 4866 4874 4882 4890 4898 4906 4914 4922 4930 4938 4946 4954 4962 4970 4978 4986 4994 5002 5010 5018 5026 5034 5042 5050 5058 5066 5074 5082 5090 5098 5106 5114 5122 5130 5138 5146 5154 5162 5170 5178 5186 5194 5202 5210 5218 5226 5234 5242 5250 5258 5266 5274 5282 5290 5298 5306 5314 5322 5330 5338 5346 5354 5362 5370 5378 5386 5394 5402 5410 5418 5426 5434 5442 5450 5458 5466 5474 5482 5490 5498 5506 5514 5522 5530 5538 5546 5554 5562 5570 5578 5586 5594 5602 5610 5618 5626 5634 5642 5650 5658 5666 5674 5682 5690 5698 5706 5714 5722 5730 5738 5746 5754 5762 5770 5778 5786 5794 5802 5810 5818 5826 5834 5842 5850 5858 5866 5874 5882 5890 5898 5906 5914 5922 5930 5938 5946 5954 5962 5970 5978 5986 5994 6002 6010 6018 6026 6034 6042 6050 6058 6066 6074 6082 6090 6098 6106 6114 6122 6130 6138 6146 6154 6162 6170 6178 6186 6194 6198 6206 6214 6222 6230 6238 6246 6254 6262 6270 6278 6286 6294 6302 6310 6318 6326 6334 6342 6350 6358 6366 6374 6382 6390 6398 6406 6414 6422 6430 6438 6446 6454 6462 6470 6478 6486 6494 6502 6510 6518 6526 6534 6542 6550 6558 6566 6574 6582 6590 6598 6606 6614 6622 6630 6638 6646 6654 6662 6670 6678 6686 6694 6702 6710 6718 6726 6734 6742 6750 6758 6766 6774 6782 6790 6798 6806 6814 6822 6830 6838 6846 6854 6862 6870 6878 6886 6894 6902 6910 6918 6926 6934 6942 6950 6958 6966 6974 6982 6990 6998 7006 7014 7022 7030 7038 7046 7054 7062 7070 7078 7086 7094 7102 7110 7118 7126 7134 7142 7150 7158 7166 7174 7182 7190 7198 7206 7214 7222 7230 7238 7246 7254 7262 7270 7278 7286 7294 7302 7310 7318 7326 7334 7342 7350 7358 7366 7374 7382 7390 7398 7406 7414 7422 7430 7438 7446 7454 7462 7470 7478 7486 7494 7502 7510 7518 7526 7534 7542 7550 7558 7566 7574 7582 7590 7598 7606 7614 7622 7630 7638 7646 7654 7662 7670 7678 7686 7694 7702 7710 7718 7726 7734 7742 7750 7758 7766 7774 7782 7790 7798 7806 7814 7822 7830 7838 7846 7854 7862 7870 7878 7886 7894 7902 7910 7918 7926 7934 7942 7950 7958 7966 7974 7982 7990 7998 8006 8014 8022 8030 8038 8046 8054 8062 8070 8078 8086 8094 8102 8110 8118 8126 8134 8142 8150 8158 8166 8174 8182 8190 8198 8206 8214 8222 8230 8238 8246 8254 8262 8270 8278 8286 8294 8302 8310 8318 8326 8334 8342 8350 8358 8366 8374 8382 8390 8398 8406 8414 8422 8430 8438 8446 8454 8462 8470 8478 8486 8494 8502 8510 8518 8526 8534 8542 8550 8558 8566 8574 8582 8590 8598 8606 8614 8622 8630 8638 8646 8654 8662 8670 8678 8686 8694 8702 8710 8718 8726 8734 8742 8750 8758 8766 8774 8782 8790 8798 8806 8814 8822 8830 8838 8846 8854 8862 8870 8878 8886 8894 8898 8906 8914 8922 8930 8938 8946 8954 8962 8970 8978 8986 8994 9002 9010 9018 9026 9034 9042 9050 9058 9066 9074 9082 9090 9098 9106 9114 9122 9130 9138 9146 9154 9162 9170 9178 9186 9194 9198 9206 9214 9222 9230 9238 9246 9254 9262 9270 9278 9286 9294 9302 9310 9318 9326 9334 9342 9350 9358 9366 9374 9382 9390 9398 9406 9414 9422 9430 9438 9446 9454 9462 9470 9478 9486 9494 9502 9510 9518 9526 9534 9542 9550 9558 9566 9574 9582 9590 9598 9606 9614 9622 9630 9638 9646 9654 9662 9670 9678 9686 9694 9702 9710 9718 9726 9734 9742 9750 9758 9766 9774 9782 9790 9798 9806 9814 9822 9830 9838 9846 9854 9862 9870 9878 9886 9894 9898 9906 9914 9922 9930 9938 9946 9954 9962 9970 9978 9986 9994 9998 0.0005 -0.0005 0.0004 -0.0022 0.0037 0.0040 -0.0022 0.0037 0.0240 0.0270 0.0064 -0.0005 0.0016 0.0012								

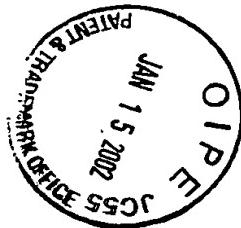


Table XIX CEA DR Super Motif Peptides with Binding

Core Sequence	SeqID Num	Core Exemplary Sequence	Exemplary SeqID Num	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
IPIWQRLLLT	1962	RWCIPWQRLLLTASL	1815	0.0110	0.0700	-0.0004			
WQRLLLT A	1963	CIPWQRLLLTASLLT	1816						
LLLTASLLT	1964	WQRLLLTASLLTFW	1817						
LLTASLLTF	1965	QRLLTASLLTFWNP	1818			-0.0013			
LTASLLTF	1966	RLLTASLLTFWNPP	1819						
LTFWNPP T	1967	ASLLTFWNPPTTAKL	1820						
PWNPPTTA	1968	LITFWNPPTTAKLTI	1821						
WNPPTTAK	1969	LTFWNPPPTTAKLIE	1822						
LTIESTPEN	1970	TAKLTIESTFVNVAE	1823						
LLVHNLPQ	1971	EVLLVHNLPQHLFG	1824	3.4000	0.4700	0.1200			
LVHNLPQH	1972	VLLVHNLPQHLFGY	1825						
YKGERV DVG	1973	YSWYKGERV DGNRQ	1826						
IGYVIGTQ	1974	NRQIGYVIGTQQAT	1827						
IGTOQATPG	1975	GYVIGTQQATPGPAY	1828						
YSGREIIY P	1976	GPA YSGREIIYPNAS	1829						
IYPNASLL	1977	GREIYPNASULLQN	1830	1.2000	0.5600	0.0083			
IYPNASLLI	1978	REIYPNASULLQNI	1831						
IYPNASLLIQ	1979	EIYPNASULLQNI	1832	0.3100	0.1600	0.0029			
LIQNIQ IQN	1980	NASLIQNIQNDTG	1833	-0.0013					
LQNIQND	1981	ASLQNIQNDTG	1834						
HQNDTG FV	1982	IONHIONDTGFTYLH	1835						
FYT LHV IKS	1983	DTGFYT LHV IKS DL V	1836	0.0009	0.1100	0.0620			
YTLHV IKS D	1984	TGF YT LHV IKS DL VN	1837						
LHV IKS DL V	1985	FYT LHV IKS DL VNEE	1838						
VIKS DL VNE	1986	TLHV IKS DL VNEEAT	1839						
IKSDL VNEE	1987	LHV IKS DL VNEEATG	1840						
LYNEEAT G	1988	KSDL VNEEATGQFRV	1841						
VNEEAT Q	1989	SDL VNEEATGQFRV	1842						
VYPELPKP	1990	QFRVYPELPKPSS	1843						
LPKPSISSN	1991	YPELPKPSSISSNSK	1844	-0.0013					
ISSNNSKPV	1992	KPSISSNNSKPVEDK	1845	0.0033					
VEDK DAVA	1993	SKPVEDK DAVA FCTE	1846						
WVNNOQLP	1994	YLWWVNNQSLPVSP	1847						
VNNQSLPV	1995	LWWVNNQSLPVSPR	1848						
LTLEFN VTR	1996	NRTLTLFVNTRNDTA	1849						
VTRNDT AS	1997	L FN VTRNDT AS YKCE	1850						
VSARR SDS	1998	ONPV SARR SDS VILN	1851						
VILVLYGP	1999	SDS VILN VLY GDPAP	1852						
LYG DAPI	2000	LNVL YGP DAPI TISPL	1853						
YGP DAP TIS	2001	NVL YGP DAPI TISPLN	1854						
ISP LNT SYR	2002	APT ISPL NT SYRS GE	1855						
LSCHA ASN	2003	NL NL SCHA ASN NPPAQ	1856						
WVYN GTFQ	2004	QYSWFVNGTFQGST	1857						
LFIPN ITVN	2005	TQELFIPN ITVN NSG	1858						
FPN ITVN N	2006	QELFIPN ITVN NSGS	1859						
IPN ITVN NS	2007	ELFIPN ITVN NSGSY	1860						

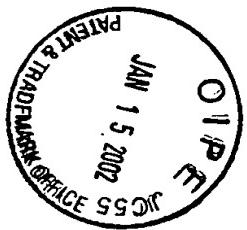


Table XIX CEA DR Super Motif Peptides with Binding

Core Sequence	SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
ITVNNSGSY	2008	IPNITVNNNSGSYTCQ	1861						
VNNSGSYT	2009	NITVNNSGSYTCQAH	1862						
LNRTTVTTI	2010	DTGUNNRRTTVTTIVY	1863						0.0088
VTTITVYAE	2011	RITVTITVYAEPPK	1864						
VYAEPKP	2012	TITVYAEPPKPFTS	1865						
ITSNNNSNPV	2013	KPFTSNNSNPVDE	1866						-0.0013
VEDEDAVA	2014	SNPVEDEDAVAVLTCE	1867						
LTLISVTR	2015	NRTLTLISVTRNDVG	1868						0.0021
VTRNDVGP	2016	LLSVTRNDVGPYECC	1869						
VGPYECGI	2017	RNDVGPYECCIQNEL	1870						
IQNELSVDH	2018	ECGIQNELSVDHSDP	1871						
LSVDHSDP	2019	QNELSVDHSDPVILN	1872						
VDHSDPVIL	2020	ELSVDHSDPVILNVL	1873						
VILNVLYGP	2021	SDPVILNVLYGDDDP	1874						
YGDDDPTIS	2022	NVLYGDDDPTISPY	1875						
ISPSYTYYR	2023	DPTISPYTYRPGV	1876						
TYYRPGV	2024	SPSYTYRPGVNL	1877						
YYPGCVNL	2025	SYTYYRPGCVNLSLSC	1878						
VNLSSLCH	2026	RPGVNLSSLCHAASN	1879						
LSCHAASN	2027	NLSLSCHAASNPPAQ	1880						
LIDGNIQHQH	2028	YSWLDGNIQHQHQE	1881						
LFIISNITEK	2029	TOELFISNITEKNSG	1882						
FISNITEKN	2030	QELFISNITEKNSGL	1883						
ITEKNSGLY	2031	ISNITEKNSGLYTQ	1884						
LYTCQANN	2032	NSGLYTQCAINAS	1885						
VKTITVSAE	2033	RTTVKTTITVSAELPK	1886						
VSAELPKP	2034	TITVSAELPKPSISS	1887						
LPKPSISSN	2035	SAELPKPSISSNNSK	1888						
WYNGQLP	2036	YLWWYNGQLPVSP	1889						
VNGQLPV	2037	LWWYNGQLPVSPR	1890						
LTLFNVTR	2038	NRTLTLFNVRNDAR	1891						
VTRNDARA	2039	LFNVRNDARAAYVC	1892						
IQNSYSAN	2040	VCGIONSYSANRSDP	1893						
VSANRSDP	2041	QNSVSANRSDPVTLQ	1894						
VTLDVLYG	2042	SDPVTLQDLYGPDTP	1895						
LYGPDTPII	2043	LDVLLYGPDTPISPP	1896						
YGPDTPIIS	2044	DVLLYGPDTPISPPD	1897						
ISPPDSSYL	2045	TPHSPPDSSYLSGA	1898						
LSGANLNL	2046	SSYLSGANLNLSCS	1899						
LSCHSASN	2047	NLNLSCHSASNPSQ	1900						
WRINGIPQQ	2048	QYSWRINGIPQQHTQ	1901						
IQOQHTQVL	2049	INGIPQQHTQVLFLIA	1902						
LFIAKITPN	2050	TQVLFLIAKITPNNING	1903						0.0038
FIAKITPN	2051	QVLFLIAKITPNNINGT	1904						0.0024
IAKITPNNN	2052	VLEIAKITPNNINGT	1905						
YACFVSNL	2053	NGTYACFVSNLATG	1906						



Table XIX

CEA DR Super Motif Peptides with Binding

Core Sequence	SeqID Num	Core Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
FVSNLATG	2054	YACFVSNLATGRNN	1907	0.0070				
VSNLATGR	2055	ACFVSNLATGRNNSI	1908					
IVSITVSA	2056	NNSIVKSITVSAASGT	1909	0.0690	0.0370	0.0120		
VSITVSA	2057	NSIVKSITVSAASGT	1910	0.0460	0.0760	0.0170		
ITVSASGT	2058	VKSITVSAASGTSPGL	1911					
VSASGTSP	2059	SITVSAASGTSPGLSA	1912					
LSAGATVGI	2060	SPGLSAGATVGIMIG	1913					
IMIGVLVGV	2061	TVGIMIGVLVGVALI	1914					
LTIESTPFN	2062	TAKLTTESTPFNVAE	1915					
YKGERVDC	2063	YSWYKGERVDCNRQ	1916					
LPVSPRLQ	2064	NQSLPVSPRLQLSNG	1917					
LNLSCHAA	2065	GENLNLSCHAAASNPP	1918					
LPVSPRLQ	2066	GQSLPVSPRLQLSNG	1919					

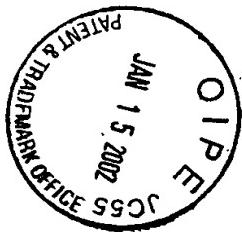


Table Xa
CEA DR 3 α Motif Peptides with Binding

Core Sequence	SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w2 β 1	DR2w2 β 2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
IQNDTGFYT	2067	QNIIQNDTGFYTLHV	1920	110	0.0044	0.0105	-	0.3200	-0.0055	-	-	-0.0008
KSDLVNEE	2068	LHVIKSDLVNEEATG	1921	122	-	-	-	0.1300	-	-	-	-
LVNEEATGQ	2069	KSDLVNEEATGQFRV	1922	126	-	-	-	0.0058	-	-	-	-
VNNEEATGQF	2070	SDLVNEEATGOFRYY	1923	127	-	-	-	-	-	-	-	-
VYPELPKPS	2071	QFRVYPELPKPSISS	1924	137	-	-	-	-	-	-	-	-
FTCEPETQD	2072	AVAFTEPEQTDATY	1925	162	-	-	-	-	-	-	-	-
YKCETQNPV	2073	TASYK CETQN PVSAR	1926	210	-	-	-	-	-	-	-	-
YGPDAPTIS	2074	NVLYGPDAPTISPLN	1927	232	-	-	-	-	-	-	-	-
VYAEPPKPF	2075	TITVYAAEPPKPFITS	1928	315	-	-	-	0.0042	-	-	-	-
VEDEDAVAL	2076	SNPVEDEDAVALTCE	1929	332	-	-	-	0.0054	-	-	-	-
LTCPEPIQN	2077	AVALTCEPEQNTTY	1930	340	-	-	-	0.0039	-	-	-	-
IQNELSYDH	2078	ECCIONEELSYDHSDP	1931	392	-	-	-	-	-	-	-	-
LSVDHSDPV	2079	QNELSVDHSDPVILN	1932	396	-	-	-	0.0820	-	-	-	-
YGDDDPITIS	2080	NVLYGPDDPITPSY	1933	410	-	-	-	-	-	-	-	-
VSAELPKPS	2081	TITVSAELPKPSISS	1934	493	-	-	-	-	-	-	-	-
FTCEPEAQN	2082	AVAFTEPEAQNTTY	1935	518	-	-	-	-	-	-	-	-
VTLDVLYQP	2083	SDPVTLDVLYGPDTIP	1936	582	-	-	-	-	-	-	-	-
YGPDTPIIS	2084	DVLYGPDTPISPPD	1937	588	-	-	-	0.0037	-	-	-	-



Table XXa CEA DR 3a Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
IQNDTGFYT	2067	QNIIQNDTGFYTLHV	1920	0.3600	-0.0017	-0.0009		
IKSDLVNEE	2068	LHVIKSDLVNEEATG	1921					
LVNEEATGQ	2069	KSDLVNEEATGQQFRV	1922					
VNEEATGQF	2070	SDLVNEEATGQFRVY	1923					
VYPELPKPS	2071	QFRVYVPELPKPSISS	1924					
FTCEPETQD	2072	AVAFTEPETQDATY	1925					
YKCETQNPKV	2073	TASYKCECQNPKVSAR	1926					
YGPDAFTIS	2074	NVLYGPDADTISPLN	1927					
VYAEPPKPF	2075	TITVVAEPPKPFITS	1928					
VEDEDAVAL	2076	SNPVDEDAVALTCE	1929					
LTCEPEIQN	2077	AVALTCEPEIQNTY	1930					
IQNELSVDH	2078	ECCIQNELSVDHSDP	1931					
LSVDHSDPV	2079	QNELSVDHSDPVLN	1932					
YGPDDPTIS	2080	NVLYGPDPTISPSY	1933					
VSAELPKPS	2081	TITVSAELPKPSISS	1934					
FTCEPEAQN	2082	AVAFTEPEAQNTTY	1935					
VTLDVLYGP	2083	SDPVTLVDVLYGPDT	1936					
YGPDTPIIS	2084	DVLYGPDPTPIISPD	1937					

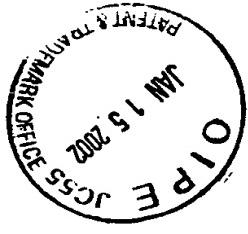


Table XXb CEA DR 3b Motif Peptides with Binding Data



Table XXb
CEA DR 3b Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9
ATGQFRVVP LNTSYRSGE YTCQAHNSD LPVSPRLQL LSNDNRLLT	2085 2086 2087 2088 2089	NEEATGGFRVVPPLP ISPLNTS'RSGENLN SGSYTCQAHNSD'TGL NOSLPVSPRLQLSDN RLQLSNDDNRTLTLLS	1938 1939 1940 1941 1942				
LSLSCHAAS LNLSCHIAS ASPETHLDM AHNQVROVP LIDTNRSA	2090 2091 2092 2093 2094	GYNLSLSCHAASNPP GANLNLSCHIASNPS RLPASPETHLDMLRH VLIJAHNQVROVPQR ALTLIDTNRSBACHP	1943 1944 1945 1946 1947	0.0048	-0.0017	-0.0009	
IHHNTHLCF LFRNPHQAL VLDLDDKGCP YLEDYRVLH IDSECRPRF	2095 2096 2097 2098 2099	LALIHHTHLCFVHT WDQLFRNPHQALLHT HSCVDLDDKGCPAEQ GMSYLEDVRLVHSDL CWMIDSECRPRFREL	1948 1949 1950 1951 1952	0.7500 0.0410	0.0200 -0.0017	0.0330 -0.0009	
AAQPQHPP AAISRKMV LHHTLKIGG IGGEPHISY AALSRKVAE	2100 2101 2102 2103 2104	QGGAAPQHPPPAFS EFQAAISRKAVELVH VKVLHHTLKIGGEPH TLKIGGEPHISTPL EFQAAISRKVAELVH	1953 1954 1955 1956 1957				
ILGDPKKLL YKOSQHME VEGNLRVEY FTLQIRGRE	2105 2106 2107 2108	EDSILGDPKKLTOH MAYKQSQHIMTEVVR LIRVEGNLRVEYLD GEVFTLQIRGRERFE	1958 1959 1960 1961	0.0130	-0.0014	0.0029	

Table XXII. Cross-reactive binding of CEA analog peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Bound
CEA.24	9	LLTFWNPPPT	2144	179	1720	67	755	-- ²	2
CEA.24M2V9	9	LMTFWNPPPV	2145	4.5	782	7.7	34	3333	3
CEA.24V9	9	LLTFWNPPPV	2146	16	307	26	56	952	4
CEA.78	9	QIIGYVIGT	2147	313	148	106	100	150	5
CEA.78L2V9	9	QLIGYVIGV	2158	9.4	5.9	2.3	21	2.3	5
CEA.233	10	VLYGPDAPTI	2149	128	606	270	804	--	2
CEA.233V10	10	VLYGPDAPTV	2150	26	430	16	206	952	4
CEA.411	10	VLYGPDDPTI	2151	294	358	476	7400	--	3
CEA.411V10	10	VLYGPDDPTV	2152	161	105	91	2467	--	3
CEA.569	9	YVCGIQNSV	2153	98	358	159	80	181	5
CEA.569L2	9	YLCGIQNSV	2154	50	24	12	31	3478	4
CEA.589	9	VLYGPDPTI	2155	200	878	53	638	--	2
CEA.589V9	9	VLYGPDTPV	2156	20	165	91	154	9756	4
CEA.605	9	YLSGANLNL	2157	28	165	2.4	804	--	3
CEA.605V9	9	YLSGANLNV	2158	73	13	13	80	1600	4
CEA.687	9	ATVGIMIGV	2159	36	8.8	20	11	0.80	5
CEA.687L2	9	ALVGIMIGV	2160	10	63	31	100	102	5
CEA.691	9	IMIGVLVGV	2161	69	62	13	106	89	5
CEA.691L2	9	ILIGVLVGV	2162	22	8.0	3.2	16	160	5

1) Wild-type peptides presented for reference purposes.

2) -- indicates binding affinity =10,000nM.

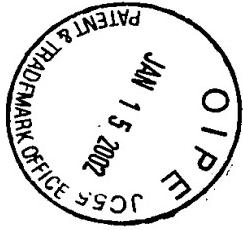


TABLE XXII A A01 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	A*0101 nM
52.0105	11	RVDGNRQIIGY	2163	CEA.72	294.1
52.0109	11	RSDSVILNVLY	2164	CEA.225	47.2
52.0113	11	HSDPVILNVLY	2165	CEA.403	25.8
52.0116	11	RSDPVTLDVLY	2166	CEA.581	7.8
57.0004	9	QQDTPGPAY	2167	CEA.87.D3	56.8
57.0007	9	AADNPPAQY	2168	CEA.261.D3	45.5
57.0008	9	ITDNNNSGSY	2169	CEA.289.D3	96.2
57.001	9	VTDNDVGPY	2170	CEA.383.D3	4.1
57.0011	9	PTDSPSYTY	2171	CEA.418.D3	37.9
57.0012	9	TIDPSYTYY	2172	CEA.419.D3	3.1
57.0013	9	AADNPPAQY	2173	CEA.439.D3	44.6
57.0014	9	ITDKNSGLY	2174	CEA.467.D3	11.9
57.0103	10	PTDSPLNTSY	2175	CEA.240.D3	266
57.0104	10	PTDSPSYTYY	2176	CEA.418.D3	1.1
57.0105	10	HTASNPSPQY	2177	CEA.616.T2	131.6
57.0106	10	HSDSNPSPQY	2178	CEA.616.D3	44.6

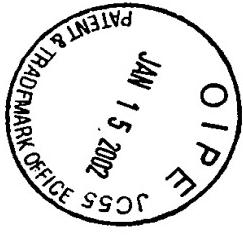


Table XII B A03 Analog Peptides

<u>Peptide</u>	<u>SEQ ID NO:</u>	<u>Source</u>	<u>A*0301 nM</u>	<u>A*1101 nM</u>	<u>A*3101 nM</u>	<u>A*3301 nM</u>	<u>A*6801 nM</u>	<u>A3 XRN</u>
1371.01	2179	CEA.241.V2	458.3	54.5	187.5	557.7	8.7	4
1371.02	2180	CEA.241.V2K10	16.9	6.3	10588.2	-48333.3	7.3	3
1371.03	2181	CEA.376.V2	343.8	222.2	11.3	6041.7	666.7	3
1371.04	2182	CEA.376.V2K10	37.9	50	163.6	-72500	5714.3	3
1371.05	2183	CEA.419.V2	2340.4	3000	29	263.6	8.6	3
1371.06	2184	CEA.419.V2K10	68.8	42.9	3673.5	26363.6	6.7	3
1371.07	2185	CEA.420.V2	91.7	13.3	25.7	58	2.6	5
1371.08	2186	CEA.420.V2K9	17.2	54.5	720	4328.4	21.6	3
1371.09	2187	CEA.554.V2	297.3	93.8	9	7631.6	42.1	4
1371.10	2188	CEA.554.V42K10	20.8	31.6	233.8	41428.6	2352.9	3
1371.11	2189	CEA.656.K9	1466.7	206.9	-36000	-72500	5.3	2
1371.13	9							

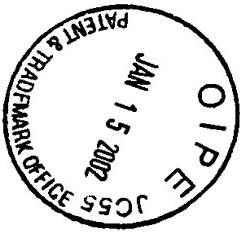


Table XXIIC A24 Analog Peptides

<u>Peptide</u>	<u>AA</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Source</u>	<u>A*2401 nM</u>
52.0033	8	IYPNASLL	2190	CEA.101	176.5
52.0038	8	SWFVNGTF	2191	CEA.270	480
52.0137	11	RWCIPWQRLLL	2192	CEA.10	151.9
52.0138	11	PWQRLLLTLASL	2193	CEA.14	324.3
52.0141	11	FYTLHVIKSDL	2194	CEA.119	480
52.0142	11	TYLWWVNQNQL	2195	CEA.175	85.7
52.0144	11	TYLWWVNQNQL	2196	CEA.353	46.2
52.0145	11	SYTYYRPGVNL	2197	CEA.423	218.2
52.0146	11	TYYRPGVNLSL	2198	CEA.425	131.9
52.0147	11	TYLWWVNQNQL	2199	CEA.531	92.3
57.0036	9	RYCIPWQRF	2200	CEA.10.Y2F9	190.5
57.0037	9	IYPNASLLF	2201	CEA.101.F9	2.2
57.0038	9	LYWVNQNQSF	2202	CEA.177.Y2F9	63.2
57.0039	9	LYGPDAPTF	2203	CEA.234.F9	63.2
57.0041	9	TYYRPGVNF	2204	CEA.425.F9	52.2
57.0042	9	LYWVNQNQSF	2205	CEA.533.Y2F9	15.8
57.0044	9	QYSWRINGF	2206	CEA.624.F9	109.1
57.0045	9	TYACFVSNF	2207	CEA.652.F9	8.6
57.0072	10	RYCIPWQRLF	2208	CEA.10.Y2F10	26.1
57.0073	10	FYNPPPTAKF	2209	CEA.27.Y2F10	181.8
57.0074	10	VYPELPKPSF	2210	CEA.140.F10	106.2
57.0075	10	TYQQSTQELF	2211	CEA.276.Y2	307.7
57.0076	10	VYAEPPKPFF	2212	CEA.318.F10	26.7
57.0077	10	YYRPGVNLSF	2213	CEA.426.F10	10
57.0078	10	QYSWLIDGNF	2214	CEA.446.F10	60
57.0079	10	SYLSGANLNF	2215	CEA.604.F10	10



Table XXIII. Immunogenicity of A2 supermotif-bearing peptides

Peptide	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*0202 nM	No. A2 Alleles Bound	CTL Peptide ¹	CTL Wild-type	CTL Tumor
CEA.78	9	QILGGYVIGT	2216	313	148	106	100	151	5	0/3		
CEA.354	10	YLWWVVNNQSL	2217	26	108	26	487	333	5	1/2	0/1	
CEA.569	9	YVCGIQNSV	2218	98	358	159	80	182	5	1/2	0/1	
CEA.605	9	YLSGANLNL	2219	28	165	2	804	-- ²	3	2/2	1/2	
CEA.687	9	ATVGIMIGV	2220	36	9	20	11	1	5	1/1	1/1	
CEA.691	9	IMIGVLVGV	2221	69	62	13	106	89	5	8/8	4/7	
CEA.24	9	LLTFWNIPPT	2222	179	1720	67	755	-- ²	2	0/1	0/1	
CEA.24V9	9	LLTFWNPPV	2223	16	307	26	56	952	4	1/1	1/1	
CEA.233	10	VLYGPDAPTI	2224	128	606	270	804	--	2	2/4	0/3	
CEA.233V10	10	VLYGPDAPTV	2225	26	430	16	206	952	4	3/4	2/2	1/4
CEA.589	9	VLYGPDTP1	2226	200	878	53	638	--	2	1/1	0/1	
CEA.589V9	9	VLYGPDTPV	2227	20	165	91	154	9756	4	2/2	2/2	0/2
CEA.605	9	YLSGANLNL	2228	28	165	24	804	--	3	2/2	1/2	
CEA.605V9	9	YLSGANLNV	2229	73	13	13	80	1600	4	4/4	3/4	1/4

1) Number of donors yielding a positive response/total tested.

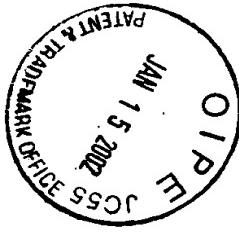
2) -- indicates binding affinity = 10,000nM.



Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

A. Class I binding assays

Species	Antigen	Allele	Cell line	Radiolabeled peptide	
				Source	Sequence
Human	A1	A*0101	Steinlin	Hu. J chain 102-110	YTAVVPLVY
	A2	A*0201	JY	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0202	P815 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0203	FUN	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0206	CLA	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0207	721.221 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV
	A3		GM3107	non-natural (A3CON1)	KVFPYALINK
A11			BVR	non-natural (A3CON1)	KVFPYALINK
A24		A*2402	KAS116	non-natural (A24CON1)	AYIDNYNKF
A31		A*3101	SPACH	non-natural (A3CON1)	KVFPYALINK
A33		A*3301	LWAGS	non-natural (A3CON1)	KVFPYALINK
A28/68		A*6801	C1R	HBVc 141-151 T7->Y	STLPETVVRR
A28/68		A*6802	AMAI	HBV pol 646-654 C4->A	FTQAGYPAL
B7		B*0702	GM3107	A2 signal seq. 5-13 (L7->Y)	APRTLVYLL
B8		B*0801	Steinlin	HIV gp 586-593 Y1->F, Q5->Y	FLKDYQLL
B27		B*2705	LG2	R 60s	FRYNGLHR
B35		B*3501	C1R, BVR	non-natural (B35CON2)	PPFKYAAAF
B35		B*3502	TISI	non-natural (B35CON2)	PPFKYAAAF
B35		B*3503	EHM	non-natural (B35CON2)	PPFKYAAAF
B44		B*4403	PITOUT	EF-1 G6->Y	AEMGKYSFY
B51		B*5301	KAS116	non-natural (B35CON2)	PPFKYAAAF
B53		B*5301	AMAI	non-natural (B35CON2)	PPFKYAAAF
B54		B*5401	KT3	non-natural (B35CON2)	PPFKYAAAF
Cw4		Cw*0401	C1R	non-natural (C4CON1)	QYDDAVYKL
Cw6		Cw*0602	721.221 transfected	non-natural (C6CON1)	YRHDDGGNVL
Cw7		Cw*0702	721.221 transfected	non-natural (C6CON1)	YRHDDGGNVL
Mouse	D ^b		EL4	Adenovirus E1A P7->Y	SGPSNTYPEI
	K ^b		EL4	VSV NP 52-59	RGYVFQGL
	D ^d		P815	HTLV-IIIB ENV G4->Y	RGPYRAFVTI
	K ^d		P815	non-natural (KdCON1)	KFNPMTKTYI
	L ^d		P815	HIVs 28-39	IPQSLDSSWTSI



B. Class II binding assays

Species	Antigen	Allele	Cell line	Radiolabeled peptide		SEQ ID NO:
				Source	Sequence	
Human	DR1	DRB1*0101	LG2	HA Y307-319	YPKYYVKQNTLKLAT	2261
	DR2	DRB1*1501	L466.1	MBP 88-102Y	VVHFFKNIVTPRTPPY	2262
	DR2	DRB1*1601	L242.5	non-natural (760.16)	YAAFAAAAAKTAAAFAA	2263
	DR3	DRB1*0301	MAT	MT 65KD Y3-13	YKTIADFDEARR	2264
	DR4w4	DRB1*0401	Preiss	non-natural (717.01)	YARFQSQTTLKQKT	2265
	DR4w10	DRB1*0402	YAR	non-natural (717.10)	YARFQRQTTLKAAAA	2266
	DR4w14	DRB1*0404	BN 40	non-natural (717.01)	YARFQSQTTLKQKT	2267
	DR4w15	DRB1*0405	KT3	non-natural (717.01)	YARFQSQTTLKQKT	2268
	DR7	DRB1*0701	Pitout	Tet. tox. 830-843	QYIKANSKFIGITE	2269
	DR8	DRB1*0802	OLL	Tet. tox. 830-843	QYIKANSKFIGITE	2270
	DR8	DRB1*0803	LUY	Tet. tox. 830-843	QYIKANSKFIGITE	2271
	DR9	DRB1*0901	HID	Tet. tox. 830-843	QYIKANSKFIGITE	2272
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843	QYIKANSKFIGITE	2273
	DR12	DRB1*1201	Herluf	unknown eluted peptide	EALIHQLKINPVYVL	2274
	DR13	DRB1*1302	H0301	Tet. tox. 830-843 S->A	QYIKANAKFIGITE	2275
	DR51	DRB5*0101	GM3107 or L416.3	Tet. tox. 830-843	QYIKANAKFIGITE	2276
	DR51	DRB5*0201	L255.1	HA 307-319	PKYVKQNTLKLAT	2277
	DRS2	DRB3*0101	MAT	Tet. tox. 830-843	NGQIGNDPNRDIL	2278
	DRS3	DRB4*0101	L257.6	non-natural (717.01)	YARFQSQTTLKQKT	2279
	DQ3.1	QAA1*0301/DQ03.1*031	PF	non-natural (ROT)	YAHAAHAAHAAHAAHAA	2280
Mouse	IA ^b		DB27.4	non-natural (ROT)	YAHAAHAAHAAHAAHAA	2281
	IA ^d	A20		non-natural (ROT)	YAHAAHAAHAAHAAHAA	2282
	IA ^t	CH-12		HEL 46-61	YNTDGSTDYGILQINSR	2283
	IA ^t	LS102.9		non-natural (ROT)	YAHAAHAAHAAHAAHAA	2284
	IA ^a	91.7		non-natural (ROT)	YAHAAHAAHAAHAAHAA	2285
	IE ^d	A20		Lambda repressor 12-26	YLEDARRKKKAYEKKK	2286
	IE ^t	CH-12		Lambda repressor 12-26	YLEDARRKKKAYEKKK	2287

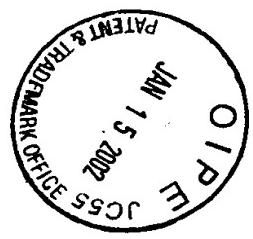


Table XXVI. Crossbinding data of A2 supermotif peptides.

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles	Crossbound
CEA.24	9	LLTFWNPP	2288	179	1720	67	755	--	2	
CEA.78	9	QIIGYYVIGT	2289	313	148	106	100	150	5	
CEA.233	10	VLYGPDAPTI	2290	128	606	270	804	--	2	
CEA.354	10	YLWWVNQNQL	2291	26	108	26	487	67	5	
CEA.411	10	VLYGPDDPTI	2292	294	358	476	7400	--	3	
CEA.432	9	NLSLSCHAA	2293	455	2867	1449	18500	--	1	
CEA.532	10	YLWWWNGQSL	2294	33	331	21	2056	286	4	
CEA.569	9	YVCGIQNSV	2295	98	358	159	80	181	5	
CEA.589	9	VLYGPDTPI	2296	200	878	53	638	--	2	
CEA.605	9	YLSGANNL	2297	28	165	2.4	804	--	3	
CEA.687	9	ATVGIMIGV	2298	36	8.8	20	11	0.80	5	
CEA.690	10	GIMIGVIVGV	2299	64	205	31	142	500	5	
CEA.691	9	IMIGVLVGV	2300	69	62	13	106	89	5	
CEA.691	10	IMIGVLVGVVA	2301	227	68	44	726	1509	3	

-- indicates binding affinity = 10,000nM.

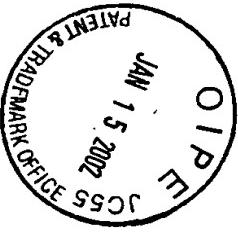


Table XXVII. Immunogenicity of A2 supermotif peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound	CTL	CTL	CTL
										Wild-type	Wild-type	Tumor
CEA.78	9	QIGGYVIGT	2302	313	148	106	100	151	5	0/3		
CEA.354	10	YLWWVVNNQSL	2303	26	108	26	487	333	5	1/2	0/1	
CEA.569	9	YVCGIQNSV	2304	98	358	159	80	182	5	1/2	0/1	
CEA.605	9	YLSGANLNL	2305	28	165	2.4	804	-- ²	3	2/2	1/2	
CEA.687	9	ATVGIMGV	2306	36	8.8	20	11	0.80	5	1/1	1/1	
CEA.691	9	IMIGVLVGV	2307	69	62	13	106	89	5	8/8	4/7	

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity = 10,000nM.

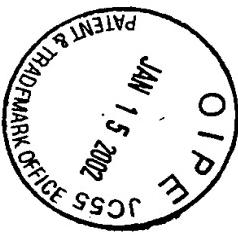


Table XXVIII. Immunogenicity A2 supermotif analog peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles	CTL Crossbound	CTL Peptide ¹	CTL Wild-type	CTL Tumor
CEA.24	9	LLTFWVNPPT	2308	179	1720	67	755	-- ²	2	2	0/1	0/1	0/1
CEA.24V9	9	LLTFWVNPPV	2309	16	307	26	56	952	4	1/1	0/1	0/1	1/1
CEA.233	10	VLYGPDAPI	2310	128	606	270	804	--	2	2	2/4	2/4	0/3
CEA.233V10	10	VLYGPDAPTV	2311	26	430	16	206	952	4	3/4	2/2	2/2	1/4
CEA.589	9	VLYGPDTPI	2312	200	878	53	638	--	2	2	1/1	1/1	0/1
CEA.589V9	9	VLYGPDTPV	2313	20	165	91	154	9756	4	2/2	2/2	2/2	0/2
CEA.605	9	YLSGANLNL	2314	28	165	2.4	804	--	3	3	2/2	2/2	1/2
CEA.605V9	9	YLSGANLNV	2315	73	13	13	80	1600	4	4/4	3/4	3/4	1/4

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity = 10,000nM.

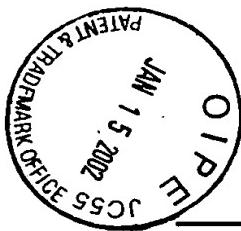


Table XXIX. DR supertype primary binding

Peptide	DR147 Algo Sum	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR147 Cross- reactivity
39.0217	2	RWCIPWQRLLLTLASL	2316	CEA.10	8.2	542	357	3
39.0218	3	QRLLLTA SLLTFWNP	2317	CEA.16	--	--	--	0
39.0219	2	EVLLL VHNLPQHLFG	2318	CEA.50	2.0	52	53	3
39.0220	3	GREIIYPNASLLIQN	2319	CEA.97	8.1	484	45	3
39.0221	2	EIIYPNASLLIQNII	2320	CEA.99	14	1154	156	2
39.0222	2	NASLLIQNIIQNDTG	2321	CEA.104	4546	--	--	0
39.0223	3	DTGFYTLHVIKSDLV	2322	CEA.116	69	1731	227	2
39.0224	2	YPELPKPSISSNNSK	2323	CEA.141	5556	--	--	0
39.0225	2	KPSISSNNNSKPVEDK	2324	CEA.146	2381	--	7576	0
39.0226	3	YLWWVNQNQLPVSPR	2325	CEA.176	0.59	8.0	42	3
39.0227	3	LWWVNQNQLPVSPRL	2326	CEA.177	217	1552	3049	1
39.0228	2	QYSWFVN GTFQQSTQ	2327	CEA.268	192	80	926	3
39.0229	2	DTGLNRTTVTTITVY	2328	CEA.305	--	--	2841	0
39.0230	2	KPFTSNNNSNPVEDE	2329	CEA.324	--	--	--	0
39.0231	2	NRTLTLLSVTRNDVG	2330	CEA.375	238	--	--	1
39.0232	2	QELFISNITEKNSGL	2331	CEA.460	--	2500	--	0
39.0233	3	RTTVKTITVSAELPK	2332	CEA.488	455	7031	317	2
39.0234	2	SAELPKPSISSNNSK	2333	CEA.497	--	--	--	0
39.0235	2	LDVLYGPDTPIISPP	2334	CEA.587	--	--	--	0
39.0236	2	TQVLFIAKITPNNNG	2335	CEA.637	61	--	6579	1
39.0237	2	QVLFIAK ITPNNNGT	2336	CEA.638	42	1875	--	1
39.0238	3	YACFVSNLATGRNNS	2337	CEA.653	208	1667	3571	1
39.0239	2	NNSIVKSITVSASGT	2338	CEA.665	91	25	676	3
39.0240	3	NSIVKSITVSASGTS	2339	CEA.666	78	25	329	3

-- indicates binding affinity =10,000nM.

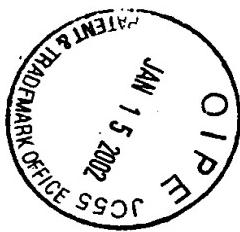


Table XXX DR supertype crossbinding

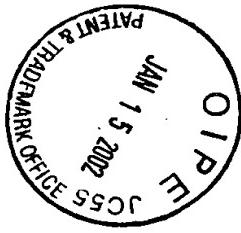
Peptide	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR2w2β1 nM	DR2w2β2 nM	DR6w19 nM	DR5w11 nM	DR8w2 nM	DR147 Degen	Broad Degen (5/8)
39.0217	RWCIPWQRLLTASL	2340	CEA.10	8.2	542	357	827	--	318	--	--	3	5
39.0219	EVLLLVHNLPQHLFG	2341	CEA.50	2.0	52	53	40	--	1.0	588	408	3	7
39.0220	GREIYPNASLIIQN	2342	CEA.97	8.1	484	45	24	8333	2.9	6897	5904	3	5
39.0221	EIYPNASHLIIQNII	2343	CEA.99	14	1154	156	57	--	11	--	--	2	4
39.0223	DTGFYTLHVIKSDLV	2344	CEA.116	69	1731	227	506	800	3889	2500	790	2	5
39.0226	YLWWVNNQSLPVSPR	2345	CEA.176	0.60	8.0	42	110	2105	2.3	29	1065	3	6
39.0228	QYSWFVNGTFQQSTQ	2346	CEA.268	192	80	926	--	6061	5833	370	--	3	4
39.0233	RTTVKTTIVSAELPK	2347	CEA.488	455	7031	317	364	--	700	--	--	2	4
39.0239	NNSIVKSITVSASGT	2348	CEA.665	91	25	676	3138	--	51	--	4083	3	4
39.0240	NSIVKSITVSASGTS	2349	CEA.666	78	25	329	3957	--	76	--	2882	3	4

-- indicates binding affinity = 10,000nM.

Table XXXI. DR3 binding

Peptide	Sequence	SEQ ID NO:	Source	DR3 nM
39.0313	QNIIQNDTGFYTLHV	2350	CEA.110	938
39.0314	LHVIKSDLVNEEATG	2351	CEA.122	2308
39.0315	KSDLVNEEATGQFRV	2352	CEA.126	--
39.0316	SDLVNEEATGQFRVY	2353	CEA.127	--
39.0317	NEEATGQFRVYPELP	2354	CEA.131	--
39.0318	QFRVYPELPKPSISS	2355	CEA.137	--
39.0319	AVAFTCPEPETQDATY	2356	CEA.162	--
39.0320	TASYKCETQNPVSAR	2357	CEA.210	--
39.0321	NVLYGPDAPTISPLN	2358	CEA.232	--
39.0322	ISPLNTSYRSGENLN	2359	CEA.242	--
39.0323	SGSYTCQAHNSDTGL	2360	CEA.294	--
39.0324	TITVYAEPPKPFITS	2361	CEA.315	--
39.0325	SNPVEDEDAVALTCE	2362	CEA.332	--
39.0326	AVALTCEPEIQNTTY	2363	CEA.340	--
39.0327	NQSLPVSPRLQLSND	2364	CEA.360	--
39.0328	RLQLSNDNRLLTLLS	2365	CEA.368	938
39.0329	ECGIQNELSVDHSDP	2366	CEA.392	--
39.0330	QNELSVDHSDPVILN	2367	CEA.396	3659
39.0331	NVLYGPDDPTISPSTY	2368	CEA.410	--
39.0332	GVNLSSLSCHAASNPP	2369	CEA.430	--
39.0333	TITVSAELPKPSISS	2370	CEA.493	--
39.0334	AVAFTCPEAQNTTY	2371	CEA.518	--
39.0335	SDPVTLVDVLYGPDT	2372	CEA.582	--
39.0336	DVLYGPDTPIISPPD	2373	CEA.588	--
39.0337	GANLNLSCHSASNPS	2374	CEA.608	--

-- indicates binding affinity =10,000nM.



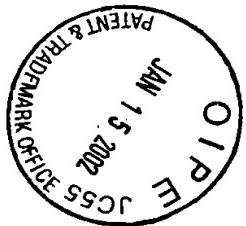


Table XXXII. HTLCandidate Epitopes

Peptide	Sequence	SEQ ID NO.	Motif	Source	DR1 nM	DR4w4 nM	DR7 nM	DR3 nM	DR2w2 81 nM	DR2w2 82 nM	DR5w1 9 nM	DR5w1 1 nM	DR8w2 nM	DR147 Cross-reactivity	Broad Cross-reactivity (5/8)	DR3 Binder
39.0217	RWCIPWQRLLL TASL	2375	DR sup	CEA.10	8.2	542	357	--	827	--	318	--	--	3	5	0
39.0219	EVLLLVHNL PQHLFG	2376	DR sup	CEA.50	2.0	52	53	336	40	--	1.0	588	408	3	7	1
39.0220	GREIYPPNASLLIQN	2377	DR sup	CEA.97	8.1	484	45	1123	24	8333	2.9	6897	5904	3	5	0
39.0313	QNIQQNDTGFYTLHV	2378	DR3	CEA.110	1136	>8182	--	938	867	--	9.7	--	--	0	2	1
39.0223	DYGFYTLHVIKSDLV	2379	DR sup	CEA.116	69	1731	227	--	506	800	3889	2500	790	2	5	0
39.0226	YLWWVVNNQSLPVSPR	2380	DR sup	CEA.176	0.60	8.0	42	2310	110	2105	2.3	29	1065	3	6	0
39.0328	RLQLSNDNRRTLTLS	2381	DR3	CEA.368	--	>8182	--	938	--	--	729	--	--	0	1	1

-- indicates binding affinity = 10,000nM.